



SEQUENCE LISTING

<110> Kapeller-Libermann, Rosana
White, David
MacBeth, Kyle J.

<120> 2786, A NOVEL HUMAN AMINOPEPTIDASE

<130> MPI99-193CN2M

<140> US 10/767,308

<141> 2004-01-29

<150> US 09/443,795

<151> 1999-11-19

<150> US 10/056,253

<151> 2002-01-24

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<211> 650

<212> PRT

<213> Homo sapiens

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 <221> misc_feature

<222> (1)...(3107)

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Leu His Ser Ala Gln Ala Val Asp Val Ala Ser Ala Ser Asn Phe Arg	
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gcc ttt gag ctg ctg cac ttg cac ctg gac ctg cgg gct gag ttc ggg	205
Ala Phe Glu Leu Leu His Leu His Leu Asp Leu Arg Ala Glu Phe Gly	
35 40 45	
cct cca ggg ccc ggc gca ggg agc cgg ggg ctg agc ggc acc gcg gtc	253
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ctg gac ctg cgc tgc ctg gag ccc gag ggc gcc gcc gag ctg cgg ctg	301
Leu Asp Leu Arg Cys Leu Glu Pro Glu Gly Ala Ala Glu Leu Arg Leu	
65 70 75 80	
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Asp Ser His Pro Cys Leu Glu Val Thr Ala Ala Ala Leu Arg Arg Glu	
85 90 95	
cgg ccc ggc tcg gag gag ccg cct gcg gag ccc gtg agc ttc tac acg	397
Arg Pro Gly Ser Glu Glu Pro Pro Ala Glu Pro Val Ser Phe Tyr Thr	
100 105 110	
cag ccc ttc tcg cac tat ggc cag gcc ctg tgc gtg tcc ttc ccg cag	445
Gln Pro Phe Ser His Tyr Gly Gln Ala Leu Cys Val Ser Phe Pro Gln	
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ccc tgc cgc gcc gcc gag cgc ctc cag gtg ctg ctc acc tac cgc gtc	493
Pro Cys Arg Ala Ala Glu Arg Leu Gln Val Leu Leu Thr Tyr Arg Val	
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Gly Glu Gly Pro Gly Val Cys Trp Leu Ala Pro Glu Gln Thr Ala Gly	
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Lys Lys Lys Pro Phe Val Tyr Thr Gln Gly Gln Ala Val Leu Asn Arg	
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Ala Phe Phe Pro Cys Phe Asp Thr Pro Ala Val Lys Tyr Lys Tyr Ser	
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gct ctt att gag gtc cca gat ggc ttc aca gct gtg atg agt gct agc	685
Ala Leu Ile Glu Val Pro Asp Gly Phe Thr Ala Val Met Ser Ala Ser	
195 200 205	
acc tgg gag aag aga ggt cca aat aag ttc ttc ttc cag atg tgt cag	733
Thr Trp Glu Lys Arg Gly Pro Asn Lys Phe Phe Phe Gln Met Cys Gln	
210 215 220	
ccc atc ccc tcc tat ctg ata gct ttg gcc atc gga gat ctg gtt tcg	781

Pro Ile Pro Ser Tyr Leu Ile Ala Leu Ala Ile Gly Asp Leu Val Ser	
225 230 235 240	
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Ala Glu Val Gly Pro Arg Ser Arg Val Trp Ala Glu Pro Cys Leu Ile	
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Thr Gly Glu Lys Leu Phe Gly Pro Tyr Val Trp Gly Arg Tyr Asp Leu	
275 280 285	
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Leu Phe Met Pro Pro Ser Phe Pro Phe Gly Gly Met Glu Asn Pro Cys	
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Leu Thr Phe Val Thr Pro Cys Leu Leu Ala Gly Asp Arg Ser Leu Ala	
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gat gtc atc atc cat gag atc tcc cac agt tgg ttt ggg aac ctg gtc	1069
Asp Val Ile Ile His Glu Ile Ser His Ser Trp Phe Gly Asn Leu Val	
325 330 335	
acc aac gcc aac tgg ggt gaa ttc tgg ctc aat gaa ggt ttc acc atg	1117
Thr Asn Ala Asn Trp Gly Glu Phe Trp Leu Asn Glu Gly Phe Thr Met	
340 345 350	
tac gcc cag agg agg atc tcc acc atc ctc ttt ggc gct gcg tac acc	1165
Tyr Ala Gln Arg Arg Ile Ser Thr Ile Leu Phe Gly Ala Ala Tyr Thr	
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Cys Leu Glu Ala Ala Thr Gly Arg Ala Leu Leu Arg Gln His Met Asp	
370 375 380	
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Ile Thr Gly Glu Glu Asn Pro Leu Asn Lys Leu Arg Val Lys Ile Glu	
385 390 395 400	
cca ggc gtt gac ccg gac gac acc tat aat gag acc ccc tac gag aaa	1309
Pro Gly Val Asp Pro Asp Asp Thr Tyr Asn Glu Thr Pro Tyr Glu Lys	
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Gly Phe Cys Phe Val Ser Tyr Leu Ala His Leu Val Gly Asp Gln Asp	
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Gln Phe Asp Ser Phe Leu Lys Ala Tyr Val His Glu Phe Lys Phe Arg	
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agc atc tta gcc gat gac ttt ctg gac ttc tac ttg gaa tat ttc cct	1453
Ser Ile Leu Ala Asp Asp Phe Leu Asp Phe Tyr Leu Glu Tyr Phe Pro	
450 455 460	
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Glu Leu Lys Lys Lys Arg Val Asp Ile Ile Pro Gly Phe Glu Phe Asp	
465 470 475 480	

cga tgg ctg aat acc ccc ggc tgg ccc ccg tac ctc cct gat ctc tcc Arg Trp Leu Asn Thr Pro Gly Trp Pro Pro Tyr Leu Pro Asp Leu Ser 485 490 495	1549
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<223> Ribonucleoprotein Binding Site	

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 Gly Ser Cys Ile Phe Tyr Leu Ile Val Ala Xaa Phe Tyr Met
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 <220>
 <223> Nuclear Localization Motif

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 <220>
 <223> Ribnucleoprotein Binding Motif

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 <223> potential catalytic site

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 <211> 4
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 <223> potential catalytic site

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